

# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	10/089,211A	
Source:	IFWID	
Date Processed by STIC:	9/17/04	

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS; PLEASE USE THE CHECKER
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<a href="http://www.uspto.gov/ebc/efs/downloads/documents.htm">http://www.uspto.gov/ebc/efs/downloads/documents.htm</a>, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal-Express, United Parcel Service, or other delivery-service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

# Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 10/089, 211A
ATTN: NEW RULES CASES:	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do <b>not</b> use tab codes between numbers; use <b>space characters</b> , instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6Patentin 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
,	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
, , ,	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number
(NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
"bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13 Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC - Biotechnology Systems Branch - 09/09/2003



IFW16

RAW SEQUENCE LISTING DATE: 09/17/2004
PATENT APPLICATION: US/10/089,211A TIME: 10:04:37

Input Set : A:\62447.txt

Output Set: N:\CRF4\09172004\J089211A.raw

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3 <110> APPLICANT: University of Victoria Innovation and Development Corporation
         Hintz, William E.
         Eades, Caleb Joshua
 7 <120> TITLE OF INVENTION: Mannosidases and Methods for using the Same
 9 <130> FILE REFERENCE: 2847-62447-01
11 <140> CURRENT APPLICATION NUMBER: 10/089,211A
12 <141> CURRENT FILING DATE: 2002-03-25
14 <150> PRIOR APPLICATION NUMBER: PCT/US00/27210
15 <151> PRIOR FILING DATE: 2000-10-02
17 <150> PRIOR APPLICATION NUMBER: 60/157,341
18 <151> PRIOR FILING DATE: 1999-10-01
                                                           Does Not Comply
20 <160> NUMBER OF SEQ ID NOS: 19
                                                       Corrected Diskette Needec
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 3328
26 <212> TYPE: DNA
27 <213> ORGANISM: Aspergillus nidulans
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32 taattetggg gaccgatate cettgaacge gggggeaate agtteaacea acceagaceg
                                                                         120
34 ctgggcttgg tatgagattg cgagcatcta tgtcggtgta ccttctgaat gacaatgaat
                                                                         180
36 gtattttact tetegaaaag aaccettggg caetgaattg tgeggagaat gatgeeetga
                                                                         240
38 ttatgataca actagtccgc tccgtcaage cacaagggtc tgggcagtcc gctataaatc
                                                                         300
40 aaaatcgcct gcacgaacag acgaataacc aagaaaacgc ccgagcgcga gcgtttcttc
                                                                         360
42 ttcctctaag cettgeaget ggetetgegt etttgateaa eeetttaget gaattteeee
                                                                         420
44 agaacttcag ccctctgcat cctgtcctta ccgcaactcg ttaacctgcg cgacctcgcg
46 cgaccacago cttaggtttc gagatgccat gaaaatcaga aattgaaccc cctttccatt
48 actatcattc tctgcattct gcgagtgatc tgtccttcga cgttccttct ttccagcgct
                                                                         600
50 geggegeett cactetegtt geetaegttt gaecaeggte etaeetetee taetgetgat
                                                                         660
52 tattaggete etecetaege etecaataea gggaagtege eggeeatgtt tegtgeaega
                                                                         720
54 cgatetegea tetegetggt gtttgeegtt atatttgtee teeteatatt ceaetttage
                                                                         780
56 cgtctcgcag ttacgatcag cctgcaatct tgggtacctc cgccgcccgt cgatcaccat
                                                                         840
58 aatcccctt teccegacca gaaceteaaa gatecatacg aaaacgacaa tagtgcgace
                                                                         900
60 ggcagtgggg ctcctccgcc tgcgttggta gagccagaag aataccaacq accaccactt
                                                                         960
62 tacacagatt cagatgacag cccaactccg tcaaaagaac gcctggacac cccgagcaat
                                                                        1020
64 gtcccatctc aggagectga atttgatgcc gccagacttc agacgggtgc gcagacccaa
                                                                        1080
66 aataaacatg aagatgatga ggatattgtc ccaatttctc actggaagec gatgcccgaa
                                                                        1140
68 eggeatecag teagteegga ggetttgate aagetgeeaa eegggeaate aaaggaaete
                                                                        1200
70 ccccaactgc aagctaagtt caaggacgag tcgtcctcgg acaagatgca qcqqctqcaa
                                                                        1260
72 caacttgaca ctatcaagte ggcgttctta catgcgtgga acggttacaa gatctctqcc
                                                                        1320
74 atgggtcatg atgaggttag acctetgcgc ggtggtttca aggacacatt caatggctgg
                                                                        1380
76 ggcgcgaccc ttgtcgacgc cttggatacc ctgtggatca tggatctcaa agaggagttc
                                                                        1440
```

78 tecatggeag tegactacgt caagaaaate gattttacca ceageaceaa gaaagagatt

1500

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/089,211A TIME: 10:04:37

DATE: 09/17/2004

Input Set : A:\62447.txt

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82 ggacacaaat acgatatact tttggaaaag tctgttgagc ttgcggatgt cttgatggac
                                                                       1620
84 gccttcgaca caccgaaccg gatgccaacc ctctattata aatggagccc agagtatgct
                                                                       1680
86 tcagagtttc gccgggggga ctttaaggct gttctcgccg agcttggctc tctctctc
                                                                       1740
88 gagttcacgc gtttggcgca gttgaccaaa caggacaagt actacgatgc aattgcacga
                                                                       1800
90 atcacaaatg agotogaaaa gtatoaggat ttgacaaago ttcccggott gtggoototo
                                                                       1860
92 aacctggacg catcegggtg caggegagtt ceeggegtet egegagagee tgetgegget
                                                                       1920
1980
96 acaagacaaa ttcatgaggg cggagagcct gtccgtcatg acaatgattc gtttgaaacg
98 ggtttteetg tateagtega taeteggaet cetececeaa ageaagattg caeeggagge
                                                                       2100
100 ctcaacgatc.agctctcagg cattgacaag ttcggactcg gagcccttgg tgactctacg
                                                                        2160
102 tacgagtact taccgaaaga gtatatgttg ctcggcggta acaacgacca gtacctcaac
                                                                        2220
104 atgtatcaga aggccatgga cacagtgcga gaatatcttg tttatcagcc aatgctcaag
                                                                        2280
106 aataategeg atgteegett ettagegaca gttagtatga caaagageet tgatgeaaac
                                                                        2340
108 ceteegggge gtaceaettt egegtaegaa ggeaeteaee teaeetgttt tgetggtggt
                                                                        2400
110 atgettgeca ttggegecaa gttgtttggg ettgataagg atetaaaget gggtagteaa
                                                                        2460
112 ctgacggacg gctgtgtctg ggcatatgaa gccacaaagt ccggaatcat qccqqaaqca
114 ttccaactgg tcccttgtaa gaaaggcgag ccatgcgaat gggatgagga cgcatactac
                                                                        2580
116 atggccatgg atccttatgc cgacaagcgg ccaatatcac ataacaaacg ctccgccggc
                                                                        2640
118 cctgaaaagg ggaattggca cgtcgtcgcc acagccgaat cgtcttcgcc ccaggaagat
                                                                        2700
120 aaaacacaga aatcaaccac tactgagggt cgacacaccg gtacaactac cggggcaggc
                                                                        2760
122 gegetetege aegaggaatt egteaeggga aaaateetea aegacegaet eeegeeggge
                                                                        2820
124 atgacaggga teteggeteg geagtacete ettegeeegg aggegatega gtetgtette
                                                                        2880
126 atcatgttcc gcctcacggg cgatccttcc tggcgcgaaa agggttggaa gatgttccag
                                                                        2940
128 gctgtcgaca aagccacgaa gacggagctg gcgaactcgg ccatttccga cgtaaccgtc
                                                                        3000
130 gataatccac geeeggtgga eagtatggaa teattetgge ttgeggagae tetgaaatae
                                                                        3060
132 ttctaccttc ttttcagcga tccaagcctg gtgagccttg acgaatatgt cttgtaagtg
                                                                        3120
134 atgettgact taategactg ettgatgetg aetttteeet taggaacace gaggeteate
                                                                        3180
136 cgttcaagcg acccaagtac tgaagtacta atttaaatga tcttttagcc tgtatctata
                                                                        3240
138 catggccgct ccgctgtaga agcattgata ccattaagac agtatcgctg cattcgtgta
                                                                        3300
140 ccatttgage ttccagagga acctettt
                                                                        3328
143 <210> SEQ ID NO: 2
                                              Per Seguerce Rules, r' can only
represent à or "g." Use n' xo
144 <211> LENGTH: 2448
145 <212> TYPE: DNA
146 <213> ORGANISM: Aspergillus nidulans
148 <220> FEATURE:
149 <221> NAME/KEY: variation
150 <222> LOCATION: (1632)..(1632)
151 <223> OTHER INFORMATION: R = A, C, G, or T
154 <400> SEQUENCE: 2
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157 atattccact ttagccgtct cgcagttacg atcagcctgc aatcttgggt acctccgccg
                                                                         120
159 cccgtcgatc accataatcc ccctttcccc gaccagaacc tcaaagatcc atacgaaaac
                                                                        180
161 gacaatagtg cgaccggcag tgggggctcct ccgcctgcgt tggtagagcc agaagaatac
                                                                         240
163 caacgaccac cactttacac agattcagat gacagcccaa ctccgtcaaa agaacgcctq
                                                                        300
165 gacaccccga gcaatgtccc atctcaggag cctgaatttg atgccgccag acttcagacg
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167 ggtgcgcaga cccaaaataa acatgaagat gatgaggata ttgtcccaat ttctcactgq
                                                                        420
169 aagccgatgc ccgaacggca tccagtcagt ccggaqqctt tqatcaaqct gccaaccqqq
                                                                        480
171 caatcaaagg aactccccca actgcaaget aagttcaagg acgagtcgtc ctcggacaag
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/089,211A

DATE: 09/17/2004 TIME: 10:04:37

Input Set : A:\62447.txt

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173 atgcagcggc tgcaacaact tgacactatc aagtcggcgt tcttacatgc gtggaacggt
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     175 tacaagatet etgecatggg teatgatgag gttagacete tgegeggtgg ttteaaggae
                                                                               660
     177 acattcaatg getggggege gaccettgte gacgeettgg ataccetgtg gatcatggat
                                                                               720
     179 ctcaaagagg agttctccat ggcagtcgac tacgtcaaga aaatcqattt taccaccage
                                                                               780
     181 accaagaaag agattccggt ctttgaaacc actattcgct acctaggcgg gatgctcggg
                                                                               840
     183 gcctatgata tttcgggaca caaatacgat atacttttgg aaaagtctgt tgagcttgcg
                                                                               900
     185 gatgtettga tggaegeett egacacaeeg aaceggatge caaceeteta ttataaatgg
                                                                               960
     187 agcccagagt atgcttcaga gtttcgccgg ggggacttta aggctgttct cgccgagctt
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     189 ggctctctct ctctcgagtt cacgcgtttg gcgcagttga ccaaacagga caagtactac
                                                                              1080
     191 gatgcaattg cacgaatcac aaatgagete gaaaagtate aggatttgac aaagetteee
                                                                              1140
     193 ggcttgtggc ctctcaacct ggacgcatcc gggtgcaggc gagttcccgg cgtctcgcga
                                                                              1200
     195 gagectgetg eggetgggea gecagteaga tggteetetg acgagateaa etegaegage
                                                                              1260
     197 tcggtatcgt atcgtacaag acaaattcat gagggcggag agcctgtccg tcatgacaat
                                                                              1320
     199 gattcgtttg aaacgggttt tcctgtatca gtcgatactc ggactcctcc cccaaagcaa
                                                                              1380
     201 gattgcaccg gaggceteaa cgatcagete teaggcattg acaagttegg acteggagee
                                                                              1440
     203 cttggtgact ctacgtacga gtacttaccg aaagagtata tgttgctcgg cggtaacaac
     205 gaccagtacc tcaacatgta tcagaaggcc atggacacag tgcgagaata tcttgtttat
     207 cagccaatgc tcaagaataa tcgcgatgtc cgcttcttag cgacagttag tatgacaaag
                                                                              1620
W--> 209 agecttgatg cnaaacetee ggggegtace actttegegt acgaaggeae teaceteace
                                                                              1680
     211 tgttttgctg gtggtatgct tgccattggc gccaagttgt ttgggcttga taaggatcta
                                                                              1740
     213 aagetgggta gtcaactgac ggacggetgt gtctgggcat atgaagecac aaagtccgga
                                                                              1800
     215 atcatgccgg aagcattcca actggtccct tgtaagaaag gcgagccatg cgaatgggat
                                                                              1860
    217 gaggacgcat actacatggc catggatect tatgccgaca ageggccaat atcacataac
                                                                              1920
    219 aaacgeteeg eeggeeetga aaaggggaat tggeaegteg tegeeacage eqaategtet
                                                                              1980
    221 tcgccccagg aagataaaac acagaaatca accactactg agggtcgaca caccggtaca
                                                                              2040
    223 actacegggg caggeget ctcgcacgag gaattcgtca cgggaaaaat cctcaacgac
                                                                              2100
    225 cgactcccgc cgggcatgac agggatctcg gctcggcagt acctccttcg cccggaggcg
                                                                              2160
    227 atcgagtctg tcttcatcat gttccgcctc acgggcgatc cttcctggcg cgaaaagggt
                                                                              2220
    229 tggaagatgt teeaggetgt egacaaagee aegaagaegg agetggegaa eteggeeatt
                                                                              2280
    231 teegaegtaa eegtegataa teeaegeeeg gtggaeagta tggaateatt etggettgeg
                                                                              2340
    233 gagactetga aataetteta eettetttte agegateeaa geetggtgag eettgaggaa
                                                                              2400
    235 tatgtcttga acaccgaggc tcatccgttc aagcgaccca ggtactga
                                                                              2448
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    239 <211> LENGTH: 815
    240 <212> TYPE: PRT
    241 <213> ORGANISM: Aspergillus nidulans
    243 <400> SEQUENCE: 3
    245 Met Phe Arg Ala Arg Arg Ser Arg Ile Ser Leu Val Phe Ala Val Ile
    249 Phe Val Leu Leu Ile Phe His Phe Ser Arg Leu Ala Val Thr Ile Ser
    253 Leu Gln Ser Trp Val Pro Pro Pro Pro Val Asp His His Asn Pro Pro
                35
    257 Phe Pro Asp Gln Asn Leu Lys Asp Pro Thr Glu Asn Asp Asn Ser Ala
    261 Thr Gly Ser Gly Ala Pro Pro Pro Ala Leu Val Glu Pro Glu Glu Thr
                            70
                                                 75
    265 Gln Arg Pro Pro Leu Thr Thr Asp Ser Asp Asp Ser Pro Thr Pro Ser
    266
                        85
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RAW SEQUENCE LISTING DATE: 09/17/2004
PATENT APPLICATION: US/10/089,211A TIME: 10:04:37

Input Set : A:\62447.txt

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269 Lys Glu Arg Leu Asp Thr Pro Ser Asn Val Pro Ser Gln Glu Pro Glu
 270
                100
                                   105
 273 Phe Asp Ala Ala Arg Leu Gln Thr Gly Ala Gln Thr Gln Asn Lys His
                    120
 277 Glu Asp Asp Glu Asp Ile Val Pro Ile Ser His Trp Lys Pro Met Pro
 278
      130
                           135
                                               140
281 Glu Arg His Pro Val Ser Pro Glu Ala Leu Ile Lys Leu Pro Thr Gly
                       150
                                          155
285 Gln Ser Lys Glu Leu Pro Gln Leu Gln Ala Lys Phe Lys Asp Glu Ser
                   165
                                      170
289 Ser Ser Asp Lys Met Gln Arg Leu Gln Gln Leu Asp Thr Ile Lys Ser
               180
                                   185
293 Ala Phe Leu His Ala Trp Asn Gly Thr Lys Ile Ser Ala Met Gly His
     195
                              200
297 Asp Glu Val Arg Pro Leu Arg Gly Gly Phe Lys Asp Thr Phe Asn Gly
                           215
                                               220
301 Trp Gly Ala Thr Leu Val Asp Ala Leu Asp Thr Leu Trp Ile Met Asp
               230
                                         235
305 Leu Lys Glu Glu Phe Ser Met Ala Val Asp Thr Val Lys Lys Ile Asp
                   245
                                       250
309 Phe Thr Thr Ser Thr Lys Lys Glu Ile Pro Val Phe Glu Thr Thr Ile
     260
                                   265
313 Arg Thr Leu Gly Gly Met Leu Gly Ala Thr Asp Ile Ser Gly His Lys
                               280
317 Thr Asp Ile Leu Leu Glu Lys Ser Val Glu Leu Ala Asp Val Leu Met
                           295
321 Asp Ala Phe Asp Thr Pro Asn Arg Met Pro Thr Leu Thr Thr Lys Trp
                       310
                                          315
325 Ser Pro Glu Thr Ala Ser Glu Phe Arg Arg Gly Asp Phe Lys Ala Val
                                      330
329 Leu Ala Glu Leu Gly Ser Leu Ser Leu Glu Phe Thr Arg Leu Ala Gln
               340
                                  345
333 Leu Thr Lys Gln Asp Lys Thr Thr Asp Ala Ile Ala Arg Ile Thr Asn
    355
                      . 360
337 Glu Leu Glu Lys Thr Gln Asp Leu Thr Lys Leu Pro Gly Leu Trp Pro
                          375
341 Leu Asn Leu Asp Ala Ser Gly Cys Arg Arg Val Pro Gly Val Ser Arg
                      390 .
                                          395
345 Glu Pro Ala Ala Ala Gly Gln Pro Val Arg Trp Ser Ser Asp Glu Ile
                  405
                                      410
349 Asn Ser Thr Ser Ser Val Ser Thr Arg Thr Arg Gln Ile His Glu Gly
              420
                                  425
353 Gly Glu Pro Val Arg His Asp Asn Asp Ser Phe Glu Thr Gly Phe Pro
     435
                              440
357 Val Ser Val Asp Thr Arg Thr Pro Pro Pro Lys Gln Asp Cys Thr Gly
                          455
                                             460
361 Gly Leu Asn Asp Gln Leu Ser Gly Ile Asp Lys Phe Gly Leu Gly Ala
                      470
365 Leu Gly Asp Ser Thr Thr Glu Thr Leu Pro Lys Glu Thr Met Leu Leu
```

RAW SEQUENCE LISTING DATE: 09/17/2004
PATENT APPLICATION: US/10/089,211A TIME: 10:04:37

Input Set : A:\62447.txt

```
485
                                         490
                                                              495
 369 Gly Gly Asn Asn Asp Gln Thr Leu Asn Met Thr Gln Lys Ala Met Asp
                 500
                       .
                                     505
 373 Thr Val Arg Glu Thr Leu Val Thr Gln Pro Met Leu Lys Asn Asn Arg
 374
             515
                                 520
 377 Asp Val Arg Phe Leu Ala Thr Val Ser Met Thr Lys Ser Leu Asp Ala
                             535
 381 Asn Pro Pro Gly Arg Thr Thr Phe Ala Thr Glu Gly Thr His Leu Thr
                         550
                                             555
 385 Cys Phe Ala Gly Gly Met Leu Ala Ile Gly Ala Lys Leu Phe Gly Leu
                     565
                                         570
389 Asp Lys Asp Leu Lys Leu Gly Ser Gln Leu Thr Asp Gly Cys Val Trp
                580
                                     585
393 Ala Thr Glu Ala Thr Lys Ser Gly Ile Met Pro Glu Ala Phe Gln Leu
                                 600
397 Val Pro Cys Lys Lys Gly Glu Pro Cys Glu Trp Asp Glu Asp Ala Thr
                             615
401 Thr Met Ala Met Asp Pro Thr Ala Asp Lys Arg Pro Ile Ser His Asn
                        630
                                             635
405 Lys Arg Ser Ala Gly Pro Glu Lys Gly Asn Trp His Val Val Ala Thr
                                         650
409 Ala Glu Ser Ser Ser Pro Gln Glu Asp Lys Thr Gln Lys Ser Thr Thr
                                     665
413 Thr Glu Gly Arg His Thr Gly Thr Thr Thr Gly Ala Gly Ala Leu Ser
                                 680
417 His Glu Glu Phe Val Thr Gly Lys Ile Leu Asn Asp Arg Leu Pro Pro
                            695
                                                 700
421 Gly Met Thr Gly Ile Ser Ala Arg Gln Thr. Leu Leu Arg Pro Glu Ala
                        710
                                             715
425 Ile Glu Ser Val Phe Ile Met Phe Arg Leu Thr Gly Asp Pro Ser Trp
                    725
                                        730
429 Arg Glu Lys Gly Trp Lys Met Phe Gln Ala Val Asp Lys Ala Thr Lys
                740
                                    745
433 Thr Glu Leu Ala Asn Ser Ala Ile Ser Asp Val Thr Val Asp Asn Pro
           755
                                .760
437 Arg Pro Val Asp Ser Met Glu Ser Phe Trp Leu Ala Glu Thr Leu Lys
                            775
441 Thr Phe Thr Leu Leu Phe Ser Asp Pro Ser Leu Val Ser Leu Glu Glu
                        790
                                            795
445 Thr Val Leu Asn Thr Glu Ala His Pro Phe Lys Arg Pro Arg Thr
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                                        810
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450 <211> LENGTH: 2177
451 <212> TYPE: DNA
452 <213> ORGANISM: Aspergillus nidulans
454 <400> SEQUENCE: 4
455 cggaatgtgc ctaaagtgga aggtatgatg atgcccagga tcgcgcccca gtcatcaact
457 ccatcatggg acggtccttg atcctcaagg cacgaagtgg agatcaggtc cgtagtgcat
                                                                          120
459 atgcatggcc catcagcetg aagcacttcc ccaagcaaag tcgagactcg gacaccgatg
```

<210> SEQ ID NO 15 <211> LENGTH: 29 <212> TYPE: DNA <213> ORGANISM: PCR Primer <220> FEATURE:	Sheet.
<pre> &lt;220&gt; FEATURE:  &lt;221&gt; NAME/KEY: y represents c, t, or u; r represents g or a; n repre  (g, t, or u; and h represents a, c, t, or u  &lt;222&gt; LOCATION: (1)(29)  &lt;223&gt; OTHER INFORMATION: Explanations gw on (2237 lise, not  &lt;400&gt; SEQUENCE: 15  ggyggyctng gygartentt ctacgagta </pre>	Ì
same enou in Sequence 16	Sequene Liles

RAW SEQUENCE LISTING ERROR SUMMARY

PATENT APPLICATION: US/10/089,211A

DATE: 09/17/2004 TIME: 10:04:38

Input Set : A:\62447.txt

Output Set: N:\CRF4\09172004\J089211A.raw

### Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 1632

Seq#:8; N Pos. 4

Seq#:15; N Pos. 9,18

Seq#:16; N Pos. 4,13,16,22,25

Invalid Line Length:

IMPORTANT ( see iten 2 on Ever Summy Steet) The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:15; Line(s) 812 Seq#:16; Line(s) 827

#### VERIFICATION SUMMARY

PATENT APPLICATION: US/10/089,211A

DATE: 09/17/2004 TIME: 10:04:38

Input Set : A:\62447.txt

Output Set: N:\CRF4\09172004\J089211A.raw

L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:1620
L:745 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:812 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:817 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:814
L:818 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:827 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:832 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:829
L:833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0